

SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Lal, Preeti  
Shah, Purvi  
Corley, Neil C.
- (ii) TITLE OF THE INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0450 US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-845-4166  
(C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: PITUNOT03  
(B) CLONE: 1760566
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Leu Leu Leu Ala
 1          5          10          15
Phe Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala
          20          25          30
Leu Glu Ala Asp Phe Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys
          35          40          45
Ala His Val Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu
          50          55          60
Val Asn Asn Leu Asn Ser Pro Ala Glu Glu Thr Gly Glu Val His Glu
65          70          75          80
Glu Glu Leu Val Ala Arg Arg Lys Leu Pro Thr Ala Leu Asp Gly Phe
          85          90          95
Ser Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu His Lys Ile Cys His
          100          105          110
Ser Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp
          115          120          125
Thr Gly Asn Asp Lys Asn Gly Lys Glu Glu Val Ile Lys Arg Lys Ile
130          135          140
Pro Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro
145          150          155          160
Tyr Ile Leu Lys Arg Asp Ser Tyr Tyr Tyr
          165          170

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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NNTCAAAGCC AGCTGAAGGA AAGAGGAAGT GCTAGAGAGA GCCCCCTTCA GTGTGCTTCT      60
GACTTTTACG GACTTGGCTT GTTAGAAGGC TGAAAGATGA TGGCAGGAAT GAAAATCCAG      120
CTTGATGCA TGCTACTCCT GGCTTTCAGC TCCTGGAGTC TGTGCTCAGA TTCAGAAGAG      180
GAAATGAAAG CATTAGAAGC AGATTTCTTG ACCAATATGC ATACATCAAA GATTAGTAAA      240
GCACATGTTC CCTCTTGGA GATGACTCTG CTAAATGTTT GCAGTCTTGT AAATAATTTG      300
AACAGCCCAG CTGAGGAAAC AGGAGAAGTT CATGAAGAGG AGCTTGTTGC AAGAAGGAAA      360
CTTCCTACTG CTTTAGATGG CTTTAGCTTG GAAGCAATGT TGACAATATA CCAGCTCCAC      420
AAAATCTGTC ACAGCAGGGC TTTTCAACAC TGGGAGTTAA TCCAGGAAGA TATTCTTGAT      480
ACTGGAATG ACAAAAATGG AAAGGAAGAA GTCATAAAGA GAAAATTCC TTATATTCTG      540
AAACGGCAGC TGTATGAGAA TAAACCCAGA AGACCTACA TACTCAAAAG AGATTCTTAC      600
TATTACTGAG AGAATAAATC ATTTATTTAC ATGTGATTGT GATTCATCAT CCCTTAATTA      660
AATATCAAAT TATATTTGTG TGAAAATGTG ACAAACACAC TTATCTGTCT CTTCTACAAT      720
TGTGGTTTAT TGAATGTGAT TTTTCTGCAC TAATATAAAT TAGACTAAGT GTTTTCAAAT      780
AAATCTAAAT CTTCAGCATG ATGTGTTGTG TATAATTGGA GTAGATATTA ATTAAGTCAC      840
CTGTATAATG TTTTGTAAAT TTGCAAAACA TATCTTGAGT TGTTTAAACA GTCAAAATGT      900
TTGATATTTT ATACCAGCTT ATGAGCTCAA AGTACTACAG CAAAGCCTAG CTGCATATC      960
ATTCACCCAA AACAAAGTAA TAGCGCCTCT TTTATTATTT TGACTGAATG TTTTATGGAA     1020
TTGAAAGAAA CATACGTTCT TTTCAAGACT TCCTCATGAA TCTCTCAATT ATAGGAAAAG     1080
TTATTGTGAT AAAATAGGAA CAGCTGAAAG ATTGATTAAT GAACATTGT TATTACTTCC     1140
TATTTTAATG AATGACATTG AACTGGATTT TTTGACCTGT TAATGGACTT GGTAGCTATT     1200
AGAAGGACAC TTGACCTCCA ATAGAAAAAA AATAAAGAAA TAAAAAGAAG TATAAAAGTA     1260
ATAAAATAAA ATCAGAAGAG AAAAAGAAAA AGAAAAGTAA AAAGAGGGGG GACACACCAT     1320
AAGAACCAAT ACCCGGGAAT TTTCGGAGCG A

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 163424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Ile Leu Leu Ala Phe
 1           5           10           15
Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala Leu
 20           25           30
Glu Thr Asp Leu Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys Ala
 35           40           45
Ser Val Pro Ser Trp Lys Met Ser Leu Leu Asn Val Cys Ser Leu Ile
 50           55           60
Asn Asn Leu Asn Ser Gln Ala Glu Glu Thr Gly Glu Phe His Glu Glu
 65           70           75           80
Glu Leu Ile Thr Arg Arg Lys Phe Pro Ala Ala Leu Asp Gly Phe Ser
 85           90           95
Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu Gln Lys Ile Cys His Ser
100           105           110
Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp Ala
115           120           125
Gly Asn Asp Lys Asn Glu Lys Glu Glu Val Ile Lys Arg Lys Ile Pro
130           135           140
Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr
145           150           155           160
Ile Leu Lys Arg Gly Ser Tyr Tyr Tyr
165
  
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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 92546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ile Gly Met Asn Leu Gln Leu Val Cys Leu Thr Leu Leu Ala Phe
 1           5           10           15
Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Asp Val Arg Ala Leu
 20           25           30
Glu Ala Asp Leu Leu Thr Asn Met His Ala Ser Lys Val Ser Lys Gly
 35           40           45
Ser Pro Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu Ile
 50           55           60
Asn Asn Leu Asn Ser Ala Ala Glu Glu Ala Gly Glu Met Arg Asp Asp
 65           70           75           80
Asp Leu Val Ala Lys Arg Lys Leu Pro Leu Val Leu Asp Asp Phe Ser
 85           90           95
  
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Leu	Glu	Ala	Leu	Leu	Thr	Val	Phe	Gln	Leu	Gln	Lys	Ile	Cys	Ser
			100					105					110	
Arg	Ala	Phe	Gln	His	Trp	Glu	Ile	Ile	Gln	Glu	Asp	Ile	Leu	Asp
		115					120					125		His
Gly	Asn	Glu	Lys	Thr	Glu	Lys	Glu	Glu	Val	Ile	Lys	Arg	Lys	Ile
	130					135					140			Pro
Tyr	Ile	Leu	Lys	Arg	Gln	Leu	Tyr	Glu	Asn	Lys	Pro	Arg	Arg	Pro
145					150					155				Tyr
Ile	Leu	Lys	Arg	Ala	Ser	Tyr	Tyr	Tyr						160
					165									